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AMENDMENTS TO THE CLAIMS

1. (Currently amended) An isolated nucleic acid molecule of a sheep type of *M. paratuberculosis* said molecule comprising ~~SEQ ID NO. 1~~ SEQ ID NO:1 or a complement thereof.

2. (Currently amended) ~~A The nucleic acid molecule of Claim 1 wherein said molecule is a probe comprising SEQ ID NO. 1 or a complement thereof.~~

3. (Currently amended) ~~A probe~~ An isolated nucleic acid molecule comprising at least 20 or more contiguous nucleotides selected from the group consisting of nucleotides 230-260 of ~~SEQ ID NO. 1~~ or SEQ ID NO: 1 and a complement thereof.

4. (Currently amended) ~~The use of a nucleic acid molecule or probe as claimed in any one of Claims 1-3~~ A method for detecting the presence of sheep types of *M. paratuberculosis* comprising, identifying the presence of at least 20 or more contiguous nucleotides of SEQ ID NO:1 or a complement thereof in the sample.

5. (Currently amended) ~~The use of SEQ ID NO. 2 or a fragment or complement thereof~~ A method for detecting the presence of cattle types of *M. paratuberculosis* comprising, identifying the presence of at least 20 or more contiguous nucleotides of SEQ ID NO:2 or a complement thereof in the sample.

6. (Currently amended) A method of distinguishing between cattle and sheep types of *M. paratuberculosis* comprising the step of identifying the presence of ~~comparing differences between~~ the nucleotide sequences of SEQ ID NO.1 and SEQ ID NO. 2 or complements of said sequences, wherein homology to SEQ ID NO:1 indicates that the *M. paratuberculosis* is of the cattle type and homology to SEQ ID NO:2 indicates that the *M. paratuberculosis* is of the sheep type.

7. (Currently amended) A method of detecting the presence of *M. paratuberculosis* in a sample via a nucleic acid amplification technique said method comprising the steps of:

- a) taking a sample from an animal or any other source;
- b) extracting nucleic acids from the sample or culturing mycobacteria from the sample and extracting nucleic acids from the mycobacterial culture;
- c) performing a nucleic acid amplification technique with one or more nucleic acid sequences ~~as claimed in Claim 1~~ wherein said amplification techniques identifies the

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presence of at least 10-12 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 1 or a complement thereof; and

d) determining the ~~identity~~ presence of *M. paratuberculosis* by the presence of the an amplification product.

8. (Currently amended) A method as claimed in Claim 7, wherein the animals ~~may include~~ are selected from the group consisting of: cattle, sheep, deer, goats, ferrets, rabbits and humans.

9. (Cancelled)

10. (Original) A method claimed in Claim 7, wherein step d) of the method comprises identifying the presence of at least 15 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 1 or a complement thereof.

11. (Original) A method as claimed in Claim 7, wherein step d) of the method comprises identifying the presence of substantially 20 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 1 or a complement thereof.

12. (Original) A method as claimed in Claim 7 step c) utilizes one oligonucleotide primer complementary to 10-12 contiguous nucleotides of SEQ ID NO. 1 or a complement thereof, and one oligonucleotide primer complementary to 10-12 nucleotides of IS900 or a complement thereof.

13. (Original) A method as claimed in Claim 7, wherein step c) utilizes one oligonucleotide primer complementary to substantially 15 contiguous nucleotides of SEQ ID NO. 1 or a complement thereof; and one oligonucleotide primer complementary to substantially 15 nucleotides of IS900 or a complement thereof.

14. (Original) A method as claimed in Claim 7, wherein step c) utilizes one oligonucleotide primer complementary to substantially 20 contiguous nucleotides of SEQ ID NO. 1 or a complement thereof, and one oligonucleotide primer complementary to substantially 20 nucleotides of IS900 or a complement thereof.

15. (Original) A method as claimed in Claim 7, wherein step d) of the method comprises identifying the presence of 10-12 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 2 or a complement thereof.

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16. **(Original)** A method as claimed in Claim 7, wherein step d) of the method comprises identifying the presence of at least 15 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 2 or a complement thereof.

17. **(Original)** A method as claimed in Claim 7, wherein step d) of the method comprises identifying the presence of approximately 20 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 2 or a complement thereof.

18. **(Original)** A method as claimed in Claim 7 wherein step c) utilizes one oligonucleotide primer complementary to 12 contiguous nucleotides of SEQ ID NO. 2 or a complement thereof, and one oligonucleotide primer complementary to 10-12 nucleotides of IS900 or a complement thereof.

19. **(Original)** A method as claimed in Claim 7, wherein step c) utilizes one oligonucleotide primer complementary to substantially 15 contiguous nucleotides of SEQ ID NO. 2 or a complement thereof; and one oligonucleotide primer complementary to substantially 15 nucleotides of IS900 or a complement thereof.

20. **(Original)** A method as claimed in Claim 7 wherein step c) utilizes one oligonucleotide primer complementary to substantially 20 contiguous nucleotides of SEQ ID NO. 2 or a complement thereof, and one oligonucleotide primer complementary to substantially 20 contiguous nucleotides of IS900 or a complement thereof.

21. **(Currently amended)** ~~The use of a probe comprising substantially 10-12 contiguous nucleotides selected from the nucleic acid comprising SEQ ID NO. 2 or a complement thereof.~~ A method to determine whether a strain of either sheep type or cattle type *M. paratuberculosis* is present in a sample, comprising:
isolating nucleic acid from said sample; and
identifying the binding of a probe comprising at least 10-12 contiguous nucleotides from SEQ ID NO: 2 or a complement thereof.

22. **(Currently amended)** ~~The use of a probe comprising~~ method of Claim 21, wherein said probe comprises at least 15 contiguous nucleotides selected from the nucleic acid comprising SEQ ID NO. 2 or a complement thereof to determine whether a strain of either sheep type or cattle type *M. paratuberculosis* is present in a sample.

23. **(Currently amended)** ~~The use of a probe comprising~~ method of Claim 22, wherein said probe comprises at least 20 contiguous nucleotides selected from the nucleic acid

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comprising SEQ ID NO. 2 or a complement thereof to determine whether a strain of either sheep type or cattle type *M. paratuberculosis* is present in a sample.

24. (Cancelled)

25. (Currently amended) ~~The use of SEQ ID NO. 1, or a fragment or complement thereof, to~~ A method to distinguish any strain of *M. paratuberculosis* from any other another strain of the MAI complex which may be present in a sample, comprising identifying the presence of SEQ ID NO:1 and/or SEQ ID NO:2 in a fragment or complement thereof in the sample, wherein the absence of said sequence indicates the absence of *M. paratuberculosis* and the presence of said sequence indicates the presence of *M. paratuberculosis*.

26. (Cancelled)

27. (Currently amended) ~~The use of SEQ ID NO. 1~~ The method of Claim 25, wherein the presence of SEQ ID NO:1 is identified, or a fragment or complement thereof, to distinguish any strain of *M. tuberculosis* complex which may be present in a sample.

28. (Currently amended) ~~The use of SEQ ID NO. 2~~ The method of Claim 25, wherein the presence of SEQ ID NO:2 is identified, or a fragment or complement thereof, to distinguish any strain of *M. tuberculosis* complex which may be present in a sample.

29. (Currently amended) ~~The use of SEQ ID NO. 1, or a fragment or complement thereof, to detect~~ The method of Claim 25, wherein the presence of *M. paratuberculosis* is identified as part of the diagnosis as a causative agent of Johne's disease or Crohn's disease.

30. (Cancelled)

31. (New) The method of Claim 4, wherein the 20 or more contiguous nucleotides are from nucleotides 230-260 of SEQ ID NO:1.